

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SCHLEGEL, C. Richard  
JENSON, A. Bennett  
GHIM, Shin-Je
- (ii) TITLE OF INVENTION: PAPILLOMAVIRUS VACCINES
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
  - (B) STREET: P.O. Box 1404
  - (C) CITY: Alexandria
  - (D) STATE: Virginia
  - (E) COUNTRY: United States
  - (F) ZIP: 22313-1404
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/724,281
  - (B) FILING DATE: 01-OCT-1996
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/004,691
  - (B) FILING DATE: 02-OCT-1995
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Teskin, Robin L.
  - (B) REGISTRATION NUMBER: 35,030
  - (C) REFERENCE/DOCKET NUMBER: 010091-015
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (703) 836-6620
  - (B) TELEFAX: (703) 836-2021

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 508 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  

Met	Tyr	Asn	Val	Phe	Gln	Met	Ala	Val	Trp	Leu	Pro	Ala	Gln	Asn	Lys
1			5						10					15	
Phe	Tyr	Leu	Pro	Pro	Gln	Pro	Ile	Thr	Arg	Ile	Leu	Ser	Thr	Asp	Glu
			20					25					30		
Tyr	Val	Thr	Arg	Thr	Asn	Leu	Phe	Tyr	His	Ala	Thr	Ser	Glu	Arg	Leu
			35				40						45		

Leu Leu Val Gly His Pro Leu Phe Glu Ile Ser Ser Asn Gln Thr Val  
 50 55 60  
 Thr Ile Pro Lys Val Ser Pro Asn Ala Phe Arg Val Phe Arg Val Arg  
 65 70 75 80  
 Phe Ala Asp Pro Asn Arg Phe Ala Phe Gly Asp Lys Ala Ile Phe Asn  
 85 90 95  
 Pro Glu Thr Glu Arg Leu Val Trp Gly Leu Arg Gly Ile Glu Ile Gly  
 100 105 110  
 Arg Gly Gln Pro Leu Gly Ile Gly Ile Thr Gly His Pro Leu Leu Asn  
 115 120 125  
 Lys Leu Asp Asp Ala Glu Asn Pro Thr Asn Tyr Ile Asn Thr His Ala  
 130 135 140  
 Asn Gly Asp Ser Arg Gln Asn Thr Ala Phe Asp Ala Lys Gln Thr Gln  
 145 150 155 160  
 Met Phe Leu Val Gly Cys Thr Pro Ala Ser Gly Glu His Trp Thr Ser  
 165 170 175  
 Arg Arg Cys Pro Gly Glu Gln Val Lys Leu Gly Asp Cys Pro Arg Val  
 180 185 190  
 Gln Met Ile Glu Ser Val Ile Glu Asp Gly Asp Met Met Asp Ile Gly  
 195 200 205  
 Phe Gly Ala Met Asp Phe Ala Ala Leu Gln Gln Asp Lys Ser Asp Val  
 210 215 220  
 Pro Leu Asp Val Val Gln Ala Thr Cys Lys Tyr Pro Asp Tyr Ile Arg  
 225 230 235 240  
 Met Asn His Glu Ala Tyr Gly Asn Ser Met Phe Phe Phe Ala Arg Arg  
 245 250 255  
 Glu Gln Met Tyr Thr Arg His Phe Phe Thr Arg Gly Gly Ser Val Gly  
 260 265 270  
 Asp Lys Glu Ala Val Pro Gln Ser Leu Tyr Leu Thr Ala Asp Ala Glu  
 275 280 285  
 Pro Arg Thr Thr Leu Ala Thr Thr Asn Tyr Val Gly Thr Pro Ser Gly  
 290 295 300  
 Ser Met Val Ser Ser Asp Val Gln Leu Phe Asn Arg Ser Tyr Trp Leu  
 305 310 315 320  
 Gln Arg Gly Gln Gly Gln Asn Asn Gly Ile Gly Trp Arg Asn Gln Leu  
 325 330 335  
 Phe Ile Thr Val Gly Asp Asn Thr Arg Gly Thr Ser Leu Ser Ile Ser  
 340 345 350  
 Met Lys Asn Asn Ala Ser Thr Thr Tyr Ser Asn Ala Asn Phe Asn Asp  
 355 360 365  
 Phe Leu Arg His Thr Glu Glu Phe Asp Leu Ser Phe Ile Val Gln Leu  
 370 375 380  
 Cys Lys Val Lys Leu Thr Pro Glu Asn Leu Ala Tyr Ile His Thr Met  
 385 390 395 400

295 Asp Pro Asn Ile Leu Glu Asp Trp Gln Leu Ser Val Ser Gln Pro Pro  
                                     405                                    410                                    415  
 Thr Asn Pro Leu Glu Asp Gln Tyr Arg Phe Leu Gly Ser Ser Leu Ala  
                                     420                                    425                                    430  
 Ala Lys Cys Pro Glu Gln Ala Pro Pro Glu Pro Gln Thr Asp Pro Tyr  
                                     435                                    440                                    445  
 Ser Gln Tyr Lys Phe Trp Glu Val Asp Leu Thr Glu Arg Met Ser Glu  
                                     450                                    455                                    460  
 Gln Leu Asp Gln Phe Pro Leu Gly Arg Lys Phe Leu Tyr Gln Ser Gly  
                                     465                                    470                                    475                                    480  
 Met Thr Gln Arg Thr Ala Thr Ser Ser Thr Thr Lys Arg Lys Thr Val  
                                     485                                    490                                    495  
 Arg Val Ser Thr Ser Ala Lys Arg Arg Arg Lys Ala  
                                     500                                    505

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 503 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Val Trp Leu Pro Ala Gln Asn Lys Phe Tyr Leu Pro Pro Gln  
 1                                    5                                    10                                    15  
 Pro Ser Thr Lys Val Leu Ser Thr Asp Glu Tyr Val Ser Arg Thr Asn  
                                     20                                    25                                    30  
 Ile Phe Tyr His Ala Ser Ser Glu Arg Leu Leu Thr Val Gly His Pro  
                                     35                                    40                                    45  
 Phe Tyr Glu Ile Tyr Lys Glu Glu Arg Ser Glu Glu Val Ile Val Pro  
                                     50                                    55                                    60  
 Lys Val Ser Pro Asn Gln Tyr Arg Val Phe Arg Leu Leu Leu Pro Asp  
                                     65                                    70                                    75                                    80  
 Pro Asn Asn Phe Ala Phe Gly Asp Lys Ser Leu Phe Asp Pro Glu Lys  
                                     85                                    90                                    95  
 Glu Arg Leu Val Trp Gly Leu Arg Gly Leu Glu Ile Gly Arg Gly Gln  
                                     100                                    105                                    110  
 Pro Leu Gly Ile Ser Val Thr Gly His Pro Thr Phe Asp Arg Tyr Asn  
                                     115                                    120                                    125  
 Asp Val Glu Asn Pro Asn Lys Asn Leu Ala Gly His Gly Gly Gly Thr  
                                     130                                    135                                    140  
 Asp Ser Arg Val Asn Met Gly Leu Asp Pro Lys Gln Thr Gln Met Phe  
                                     145                                    150                                    155                                    160  
 Met Ile Gly Cys Lys Pro Ala Leu Gly Glu His Trp Ser Leu Thr Arg  
                                     165                                    170                                    175

Trp Cys Thr Gly Gln Val His Thr Ala Gly Gln Cys Pro Pro Ile Glu  
 180 185 190  
 Leu Arg Asn Thr Thr Ile Glu Asp Gly Asp Met Val Asp Ile Gly Phe  
 195 200 205  
 Gly Ala Met Asp Phe Lys Ala Leu Gln His Tyr Lys Ser Gly Val Pro  
 210 215 220  
 Ile Asp Ile Val Asn Ser Ala Cys Lys Tyr Pro Asp Tyr Leu Lys Met  
 225 230 235 240  
 Ala Asn Glu Pro Tyr Gly Asp Arg Cys Phe Phe Phe Val Arg Arg Glu  
 245 250 255  
 Gln Leu Tyr Ala Arg His Ile Met Ser Arg Ser Gly Thr Gln Gly Leu  
 260 265 270  
 Glu Pro Val Pro Lys Asp Thr Tyr Ala Thr Arg Glu Asp Asn Asn Ile  
 275 280 285  
 Gly Thr Thr Asn Tyr Phe Ser Thr Pro Ser Gly Ser Leu Val Ser Ser  
 290 295 300  
 Glu Gly Gln Leu Phe Asn Arg Pro Tyr Trp Ile Gln Arg Ser Gln Gly  
 305 315 320  
 Lys Asn Asn Gly Ile Ala Trp Gly Asn Gln Leu Phe Leu Thr Val Val  
 325 330 335  
 Asp Asn Thr Arg Gly Thr Pro Leu Thr Ile Asn Ile Gly Gln Gln Asp  
 340 345 350  
 Lys Pro Glu Glu Gly Asn Tyr Val Pro Ser Ser Tyr Arg Thr Tyr Leu  
 355 360 365  
 Arg His Val Glu Glu Tyr Glu Val Ser Ile Ile Val Gln Leu Cys Lys  
 370 375 380  
 Val Lys Leu Ser Pro Glu Asn Leu Ala Ile Ile His Thr Met Asp Pro  
 385 390 395 400  
 Asn Ile Ile Glu Asp Trp His Leu Asn Val Thr Pro Pro Ser Gly Thr  
 405 410 415  
 Leu Asp Asp Thr Tyr Arg Tyr Ile Asn Ser Leu Ala Thr Lys Cys Pro  
 420 425 430  
 Thr Asn Ile Pro Pro Lys Thr Asn Val Asp Pro Phe Arg Asp Phe Lys  
 435 440 445  
 Phe Trp Glu Val Asp Leu Lys Asp Lys Met Thr Glu Gln Leu Asp Gln  
 450 455 460  
 Thr Pro Leu Gly Arg Lys Phe Leu Phe Gln Thr Asn Val Leu Arg Arg  
 465 470 475 480  
 Arg Ser Val Lys Val Arg Ser Thr Ser His Val Ser Val Lys Arg Lys  
 485 490 495  
 Ala Val Lys Arg Lys Arg Lys  
 500